In the specification:

Please amend the specification as follows:

Please delete the paragraph on page 2, lines 16-22 and replace it with the following paragraph:

Figure 1 depicts an alignment of the amino acid sequences of the PRSS11-L protein **(SEQ ID NO: 2)** and the two other S2 serine proteases, PRSS11 **(SEQ ID NO: 9)** (Genbank Protein ID: CAA69226) and Omi **(SEQ ID NO: 10)** (Genbank Protein ID: AAB94569). The alignment was performed using the Wisconsin GCG Gap Needleman and Wunsch algorithm. The active site residues of the catalytic triad are indicated above the sequences by asterisks (*).

Please delete the paragraph on page 2, lines 23-26 and replace it with the following paragraph:

Figure 2 depicts an alignment of the amino acid sequences of the PRSS11-L protein **(SEQ ID NO: 2)** and HtrA3 **(SEQ ID NO: 11)** (Genbank Protein ID: AAH34390). The alignment was performed using the Wisconsin GCG Gap Needleman and Wunsch algorithm.

Please delete the paragraph on page 3, lines 5-7 and replace it with the following paragraph:

Figure 4 shows the splice donor/acceptor sites for human HtrA3 and PRSS11-L transcripts on the HtrA3 gene. E stands for exon. **Figure discloses SEQ ID NOS: 12-29, respectively, in order of appearance.**

Please delete the paragraph on page 13, lines 11-27, and replace it with the following paragraph:

A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin et al., (1990), Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin et al., (1993), Proc. Natl. Acad. Sci. USA 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al., (1990), J. Mol. Biol 215:403-410. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in

Altschul et al., (1997), Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. ~~See http://www.ncbi.nlm.nih.gov.~~ Additionally, there is the FASTA method (Atschul et al., (1990), J. Molec. Biol. 215, 403), which can be used.

Please delete the paragraph on page 79, lines 3-25 and replace it with the following paragraph:

Sequence alignment revealed that PRSS11-L protein shared strong homology to the catalytic domains of the other two human S2 serine proteases (Fig. 1). Motifs shared by all three human S2 serine proteases are TNAHVV **(SEQ ID NO: 30)**, DIA and GNSGGPLVNLDGEVIG **(SEQ ID NO: 31)** within the catalytic domains with the catalytic triad residues H, D and S of protease PRSS11-L located at positions 72, 108 and 186, respectively (using the methionine initiator of the PRSS11-L sequence as number one) (Fig. 1). In addition, the catalytic domains of these three S2 proteases appears to be flanked by an SH3 domain at the amino terminus and a PDZ domain at the C-terminus, both domains are importantly involved protein-interaction (Mayer, (2000), *J. Cell Science* 114: 1253-1263; Sheng et al., (2001), *Annu. Rev. Neurosci.* 24:1-29). Therefore, PRSS11-L can interact with other proteins through these interactions interfaces. It is formally possible that the PRSS11-L protein is initially synthesized as an inactive zymogen precursor, which requires one or more limitedc proteolytic cleavages to become active. Because PRSS11-L protein appears to lack any hydrophobic amino acid stretch consistent with either a signal sequence or transmembrane domain, it is not likely to be secreted or an integral membrane protein.